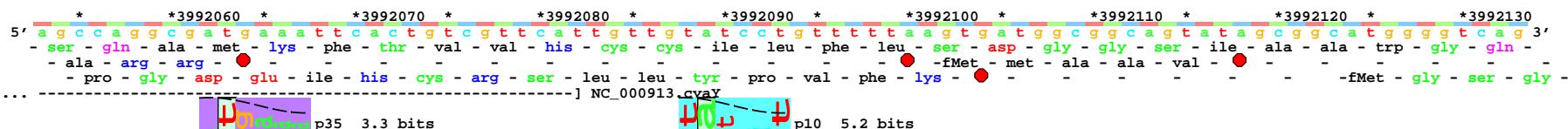
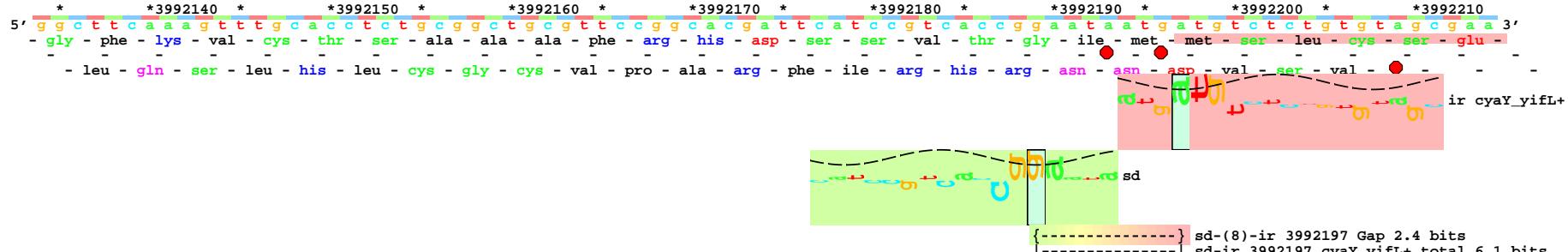


- 1 -

piece 1, NC_000913, cyaY_yifL+, config: linear, direction: +, begin: 3992053, end: 3992564



p35-(26)-p1_3992089 Gap 3.7 bits
p35-p10_3992089 total 4.9 bits



The diagram illustrates a bacterial promoter region with the following features:

- Genomic Context:** The sequence starts with a 5' end at the top and ends with a 3' end at the bottom.
- Transcription Start Sites:** Indicated by asterisks (*).
- Protein Coding:** Below the sequence, amino acid sequences are listed for several genes, separated by dashed lines.
- Regulatory Elements:**
 - p35:** A purple box representing a Pribnow box (sigma-70 promoter) located upstream of the first gene. It is labeled "p35 5.6 bits".
 - p10:** Two light blue boxes representing Pribnow boxes (sigma-S70 promoters) located upstream of the second gene. The first is labeled "p10 1.5 bits" and the second is labeled "p10 6.4 bits".
 - sd:** A green box representing a sigma-D promoter located downstream of the second gene. It is labeled "sd".
 - ir:** A red box representing an inverted repeat sequence located downstream of the second gene. It is labeled "ir cyaY_yifL".
 - Gap Regions:** Labeled as "Gap 1.4 bits" between p35 and p10, and "Gap 2.3 bits" between sd and ir.
- Other Features:** Red dots indicate specific mutations or binding sites within the sequence.

p35 3.8 bits
{-----} p35-(22)-p10 3992276 Gap 2.3 bit
----- p35-p10 3992276 total 7.9 bits

{ ... p35-(23)-p10 3992473 Gap
| ... p35-p10 3992473 total 4.3

